

SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA

<120> NOVEL bHLH TYPE TRANSCRIPTION FACTOR GENES DEC2

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<150> JP 1999-233286

<151> 1999-08-19

<160> 16

<170> PatentIn Ver. 2.1

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<211> 3641

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (135).. (1580)

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aacagcagtt gaac atg gac gaa gga att cct cat ttg caa gag aga cag 170

Met Asp Glu Gly Ile Pro His Leu Gln Glu Arg Gln

1

5

10

tta ctg gaa cat aga gat ttt ata gga ctg gac tat tcc tct ttg tat 218

Leu Leu Glu His Arg Asp Phe Ile Gly Leu Asp Tyr Ser Ser Leu Tyr

15

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25

atg tgt aaa ccc aaa agg agc atg aaa cga gac gac acc aag gat acc 266

Met Cys Lys Pro Lys Arg Ser Met Lys Arg Asp Asp Thr Lys Asp Thr

30

35

40

tac aaa tta ccg cac aga tta ata gaa aag aaa aga aga gac cga att 314

Tyr Lys Leu Pro His Arg Leu Ile Glu Lys Lys Arg Arg Asp Arg Ile

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aat gaa tgc att gct cag ctg aaa gat tta ctg cct gaa cat ctg aaa 362

Asn Glu Cys Ile Ala Gln Leu Lys Asp Leu Leu Pro Glu His Leu Lys

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70

75

ttg aca act ctg gga cat ctg gag aaa gct gta gtc ttg gaa tta act 410

Leu Thr Thr Leu Gly His Leu Glu Lys Ala Val Val Leu Glu Leu Thr

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ttg aaa cac tta aaa gct tta acc gcc tta acc gag caa cag cat cag 458

Leu Lys His Leu Lys Ala Leu Thr Ala Leu Thr Glu Gln Gln His Gln

95

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aag ata att gct tta cag aat ggg gag cga tct ctg aaa tcg ccc att 506

Lys Ile Ile Ala Leu Gln Asn Gly Glu Arg Ser Leu Lys Ser Pro Ile

110

115

120

cag tcc gac ttg gat gcg ttc cac tcg gga ttt caa aca tgc gcc aaa 554

Gln Ser Asp Leu Asp Ala Phe His Ser Gly Phe Gln Thr Cys Ala Lys

125

130

135

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gaa gtc ttg caa tac ctc tcc cgg ttt gag agc tgg aca ccc agg gag 602

Glu Val Leu Gln Tyr Leu Ser Arg Phe Glu Ser Trp Thr Pro Arg Glu

145

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155

ccg cgg tgt gtc cag ctg atc aac cac ttg cac gcc gtg gcc acc cag 650

Pro Arg Cys Val Gln Leu Ile Asn His Leu His Ala Val Ala Thr Gln

160

165

170

ttc ttg ccc acc ccg cag ctg ttg act caa cag gtc cct ctg agc aaa 698

Phe Leu Pro Thr Pro Gln Leu Leu Thr Gln Gln Val Pro Leu Ser Lys

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185

ggc acc ggc gct ccc tcg gcc gcc ggg tcc gcg gcc gcc ccc tgc ctg 746

Gly Thr Gly Ala Pro Ser Ala Ala Gly Ser Ala Ala Ala Pro Cys Leu

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Glu Arg Ala Gly Gln Lys Leu Glu Pro Leu Ala Tyr Cys Val Pro Val

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atc cag cgg act cag ccc agc gcc gag ctc gcc gcc gag aac gac acg 842

Ile Gln Arg Thr Gln Pro Ser Ala Glu Leu Ala Ala Glu Asn Asp Thr

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230

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gac acc gac agc ggc tac ggc ggc gaa gcc gag gcc cgg ccg gac cgc 890

Asp Thr Asp Ser Gly Tyr Gly Gly Glu Ala Glu Ala Arg Pro Asp Arg

240

245

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gag aaa ggc aaa ggc gcg ggg gcg agc cgc gtc acc atc aag cag gag 938

Glu Lys Gly Lys Gly Ala Gly Ala Ser Arg Val Thr Ile Lys Gln Glu

255

260

265

cct ccc ggg gag gac tcg ccg gcg ccc aag agg atg aag ctg gat tcc 986

Pro Pro Gly Glu Asp Ser Pro Ala Pro Lys Arg Met Lys Leu Asp Ser

270

275

280

cgc ggc ggc ggc agc ggc ggc ggc ccg ggg ggc ggc gcg gcg gcg gcg 1034

Arg Gly Gly Gly Ser Gly Gly Gly Pro Gly Gly Gly Ala Ala Ala Ala

285 290 295 300

gca gcc gcg ctt ctg ggg ccc gac cct gcc gcc gcg gcc gcg ctg ctg 1082

Ala Ala Ala Leu Leu Gly Pro Asp Pro Ala Ala Ala Ala Ala Leu Leu

305 310 315

aga ccc gac gcc gcc ctg ctc agc tcg ctg gtg gcg ttc ggc gga ggc 1130

Arg Pro Asp Ala Ala Leu Leu Ser Ser Leu Val Ala Phe Gly Gly Gly

320 325 330

gga ggc gcg ccc ttc ccg cag ccc gcg gcc gcc gcg gcc ccc ttc tgc 1178

Gly Gly Ala Pro Phe Pro Gln Pro Ala Ala Ala Ala Ala Pro Phe Cys

335 340 345

ctg ccc ttc tgc ttc ctc tcg cct tct gca gct gcc gcc tac gtg cag 1226

Leu Pro Phe Cys Phe Leu Ser Pro Ser Ala Ala Ala Ala Tyr Val Gln

350 355 360

ccc ttc ctg gac aag agc ggc ctg gag aag tat ctg tac ccg gcg gcg 1274

Pro Phe Leu Asp Lys Ser Gly Leu Glu Lys Tyr Leu Tyr Pro Ala Ala

365 370 375 380

gct gcc gcc ccg ttc ccg ctg cta tac ccc ggc atc ccc gcc ccg gcg 1322

Ala Ala Ala Pro Phe Pro Leu Leu Tyr Pro Gly Ile Pro Ala Pro Ala

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Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Phe

400

405

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ccc tgc ctg tcc tcg gtg ttg tcg ccc cct ccc gag aag gcg ggc gcc 1418

Pro Cys Leu Ser Ser Val Leu Ser Pro Pro Pro Glu Lys Ala Gly Ala

415

420

425

gcc gcc gcg acc ctc ctg ccg cac gag gtg gcg ccc ctt ggg gcg ccg 1466

Ala Ala Ala Thr Leu Leu Pro His Glu Val Ala Pro Leu Gly Ala Pro

430

435

440

cac ccc cag cac ccg cac ggc cgc acc cac ctg ccc ttc gcc ggg ccc 1514

His Pro Gln His Pro His Gly Arg Thr His Leu Pro Phe Ala Gly Pro

445

450

455

460

cgc gag ccg ggg aac ccg gag agc tct gct cag gaa gat ccc tcg cag 1562

Arg Glu Pro Gly Asn Pro Glu Ser Ser Ala Gln Glu Asp Pro Ser Gln

465

470

475

cca gga aag gaa gct ccc tgaatccttg cgtcccgaag gacggaggtt 1610

Pro Gly Lys Glu Ala Pro

480

1610
gacggaggtt
cgtcccgaag
tgaatccttg
ccc
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aag
gga
cca

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<211> 482

<212> PRT

<213> Homo sapiens

<400> 2

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15

Arg Asp Phe Ile Gly Leu Asp Tyr Ser Ser Leu Tyr Met Cys Lys Pro

20

25

30

Lys Arg Ser Met Lys Arg Asp Asp Thr Lys Asp Thr Tyr Lys Leu Pro

35

40

45

His Arg Leu Ile Glu Lys Lys Arg Arg Asp Arg Ile Asn Glu Cys Ile

50

55

60

Ala Gln Leu Lys Asp Leu Leu Pro Glu His Leu Lys Leu Thr Thr Leu

65

70

75

80

Gly His Leu Glu Lys Ala Val Val Leu Glu Leu Thr Leu Lys His Leu

85

90

95

Lys Ala Leu Thr Ala Leu Thr Glu Gln Gln His Gln Lys Ile Ile Ala

100

105

110

Leu Gln Asn Gly Glu Arg Ser Leu Lys Ser Pro Ile Gln Ser Asp Leu

115

120

125

Asp Ala Phe His Ser Gly Phe Gln Thr Cys Ala Lys Glu Val Leu Gln

130

135

140

Tyr Leu Ser Arg Phe Glu Ser Trp Thr Pro Arg Glu Pro Arg Cys Val

145	150	155	160
Gln Leu Ile Asn His Leu His Ala Val Ala Thr Gln Phe Leu Pro Thr			
	165	170	175
Pro Gln Leu Leu Thr Gln Gln Val Pro Leu Ser Lys Gly Thr Gly Ala			
	180	185	190
Pro Ser Ala Ala Gly Ser Ala Ala Ala Pro Cys Leu Glu Arg Ala Gly			
	195	200	205
Gln Lys Leu Glu Pro Leu Ala Tyr Cys Val Pro Val Ile Gln Arg Thr			
	210	215	220
Gln Pro Ser Ala Glu Leu Ala Ala Glu Asn Asp Thr Asp Thr Asp Ser			
225	230	235	240
Gly Tyr Gly Gly Glu Ala Glu Ala Arg Pro Asp Arg Glu Lys Gly Lys			
	245	250	255
Gly Ala Gly Ala Ser Arg Val Thr Ile Lys Gln Glu Pro Pro Gly Glu			
	260	265	270
Asp Ser Pro Ala Pro Lys Arg Met Lys Leu Asp Ser Arg Gly Gly Gly			
	275	280	285

Ser Gly Gly Gly Pro Gly Gly Gly Ala Ala Ala Ala Ala Ala Ala Leu

290

295

300

Leu Gly Pro Asp Pro Ala Ala Ala Ala Ala Leu Leu Arg Pro Asp Ala

305

310

315

320

Ala Leu Leu Ser Ser Leu Val Ala Phe Gly Gly Gly Gly Gly Ala Pro

325

330

335

Phe Pro Gln Pro Ala Ala Ala Ala Ala Pro Phe Cys Leu Pro Phe Cys

340

345

350

Phe Leu Ser Pro Ser Ala Ala Ala Ala Tyr Val Gln Pro Phe Leu Asp

355

360

365

Lys Ser Gly Leu Glu Lys Tyr Leu Tyr Pro Ala Ala Ala Ala Ala Pro

370

375

380

Phe Pro Leu Leu Tyr Pro Gly Ile Pro Ala Pro Ala Ala Ala Ala Ala

385

390

395

400

Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Phe Pro Cys Leu Ser

405

410

415

Ser Val Leu Ser Pro Pro Pro Glu Lys Ala Gly Ala Ala Ala Ala Thr

420

425

430

Leu Leu Pro His Glu Val Ala Pro Leu Gly Ala Pro His Pro Gln His

435

440

445

Pro His Gly Arg Thr His Leu Pro Phe Ala Gly Pro Arg Glu Pro Gly

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Asn Pro Glu Ser Ser Ala Gln Glu Asp Pro Ser Gln Pro Gly Lys Glu

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470

475

480

Ala Pro

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially

Synthesized Primer Sequence

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<210> 4

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 4

gcaagtgggtt gatcagctgg acaca

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<210> 5

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 5

gcttaccat acgatgttcc a

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<210> 6

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 6

tggaacgcat ccaagtcgga ctgaat

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<210> 7

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

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ttgaacatgg acgaaggaat tcc

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<210> 8

<211> 32

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

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gagatggtgc acgatgcaca gttgaagtga ac

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<210> 9

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

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attcagtcgcg acttgatgc gttcca

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<210> 10

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially

Synthesized Primer Sequence

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gcgggggtttt tcagtatcta cga

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<210> 11

<211> 1511

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2)..(1453)

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Met Asp Glu Gly Ile Pro His Leu Gln Glu Arg Gln Leu Leu Glu His

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15

aga gat ttt ata gga ctg gac tat tcc tct ttg tat atg tgt aaa ccc 97

Arg Asp Phe Ile Gly Leu Asp Tyr Ser Ser Leu Tyr Met Cys Lys Pro

20

25

30

aaa agg agc atg aaa cga gac gac acc aag gta agt gat acc tac aaa 145

Lys Arg Ser Met Lys Arg Asp Asp Thr Lys Val Ser Asp Thr Tyr Lys

35

40

45

tta ccg cac aga tta ata gaa aag aaa aga aga gac cga att aat gaa 193

Leu Pro His Arg Leu Ile Glu Lys Lys Arg Arg Asp Arg Ile Asn Glu

50

55

60

tgc att gct cag ctg aaa gat tta ctg cct gaa cat ctg aaa ttg aca 241

Cys Ile Ala Gln Leu Lys Asp Leu Leu Pro Glu His Leu Lys Leu Thr

65

70

75

80

act ctg gga cat ctg gag aaa gct gta gtc ttg gaa tta act ttg aaa 289

Thr Leu Gly His Leu Glu Lys Ala Val Val Leu Glu Leu Thr Leu Lys

85

90

95

cac tta aaa gct tta acc gcc tta acc gag caa cag cat cag aag ata 337

His Leu Lys Ala Leu Thr Ala Leu Thr Glu Gln Gln His Gln Lys Ile

100

105

110

att gct tta cag aat ggg gag cga tct ctg aaa tcg ccc att cag tcc 385

Ile Ala Leu Gln Asn Gly Glu Arg Ser Leu Lys Ser Pro Ile Gln Ser

115

120

125

gac ttg gat gcg ttc cac tcg gga ttt caa aca tgc gcc aaa gaa gtc 433

Asp Leu Asp Ala Phe His Ser Gly Phe Gln Thr Cys Ala Lys Glu Val

130

135

140

ttg caa tac ctc tcc cgg ttt gag agc tgg aca ccc agg gag ccg cgg 481

Leu Gln Tyr Leu Ser Arg Phe Glu Ser Trp Thr Pro Arg Glu Pro Arg

145

150

155

160

tgt gtc cag ctg atc aac cac ttg cac gcc gtg gcc acc cag ttc ttg 529

Cys Val Gln Leu Ile Asn His Leu His Ala Val Ala Thr Gln Phe Leu

165

170

175

ccc acc ccg cag ctg ttg act caa cag gtc cct ctg agc aaa ggc acc 577

Pro Thr Pro Gln Leu Leu Thr Gln Gln Val Pro Leu Ser Lys Gly Thr

180

185

190

ggc gct ccc tcg gcc gcc ggg tcc gcg gcc gcc ccc tgc ctg gag cgc 625

Gly Ala Pro Ser Ala Ala Gly Ser Ala Ala Ala Pro Cys Leu Glu Arg

195

200

205

gcg ggg cag aag ctg gag ccc ctc gcc tac tgc gtg ccc gtc atc cag 673

Ala Gly Gln Lys Leu Glu Pro Leu Ala Tyr Cys Val Pro Val Ile Gln

210

215

220

cgg act cag ccc agc gcc gag ctc gcc gcc gag aac gac acg gac acc 721

Arg Thr Gln Pro Ser Ala Glu Leu Ala Ala Glu Asn Asp Thr Asp Thr

225

230

235

240

gac agc ggc tac ggc ggc gaa gcc gag gcc cgg ccg gac cgc gag aaa 769

Asp Ser Gly Tyr Gly Gly Glu Ala Glu Ala Arg Pro Asp Arg Glu Lys

245

250

255

ggc aaa ggc gcg ggg gcg agc cgc gtc acc atc aag cag gag cct ccc 817

Gly Lys Gly Ala Gly Ala Ser Arg Val Thr Ile Lys Gln Glu Pro Pro

260

265

270

ggg gag gac tcg ccg gcg ccc aag agg atg aag ctg gat tcc cgc ggc 865

Gly Glu Asp Ser Pro Ala Pro Lys Arg Met Lys Leu Asp Ser Arg Gly

275

280

285

ggc ggc agc ggc ggc ggc ccg ggg ggc ggc gcg gcg gcg gcg gca gcc 913

Gly Gly Ser Gly Gly Gly Pro Gly Gly Gly Ala Ala Ala Ala Ala Ala

290

295

300

gcg ctt ctg ggg ccc gac cct gcc gcc gcg gcc gcg ctg ctg aga ccc 961

Ala Leu Leu Gly Pro Asp Pro Ala Ala Ala Ala Ala Leu Leu Arg Pro

305

310

315

320

gac gcc gcc ctg ctc agc tcg ctg gtg gcg ttc ggc gga ggc gga ggc 1009

Asp Ala Ala Leu Leu Ser Ser Leu Val Ala Phe Gly Gly Gly Gly Gly

325

330

335

gcg ccc ttc ccg cag ccc gcg gcc gcc gcg gcc ccc ttc tgc ctg ccc 1057

Ala Pro Phe Pro Gln Pro Ala Ala Ala Ala Ala Pro Phe Cys Leu Pro

340

345

350

ttc tgc ttc ctc tcg cct tct gca gct gcc gcc tac gtg cag ccc ttc 1105

Phe Cys Phe Leu Ser Pro Ser Ala Ala Ala Ala Tyr Val Gln Pro Phe

355

360

365

ctg gac aag agc ggc ctg gag aag tat ctg tac ccg gcg gcg gct gcc 1153

Leu Asp Lys Ser Gly Leu Glu Lys Tyr Leu Tyr Pro Ala Ala Ala Ala

370

375

380

gcc ccg ttc ccg ctg cta tac ccc ggc atc ccc gcc ccg gcg gca gcc 1201

Ala Pro Phe Pro Leu Leu Tyr Pro Gly Ile Pro Ala Pro Ala Ala Ala

385

390

395

400

gcg gca gcc gcc gcc gcc gct gcc gcc gcc gcc gcc gcg ttc ccc tgc 1249

Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Phe Pro Cys

405

410

415

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Leu Ser Ser Val Leu Ser Pro Pro Pro Glu Lys Ala Gly Ala Ala Ala

420

425

430

gcg acc ctc ctg ccg cac gag gtg gcg ccc ctt ggg gcg ccg cac ccc 1345

Ala Thr Leu Leu Pro His Glu Val Ala Pro Leu Gly Ala Pro His Pro

435

440

445

cag cac ccg cac ggc cgc acc cac ctg ccc ttc gcc ggg ccc cgc gag 1393

Gln His Pro His Gly Arg Thr His Leu Pro Phe Ala Gly Pro Arg Glu

450

455

460

ccg ggg aac ccg gag agc tct gct cag gaa gat ccc tcg cag cca gga 1441

Pro Gly Asn Pro Glu Ser Ser Ala Gln Glu Asp Pro Ser Gln Pro Gly

465

470

475

480

aag gaa gct ccc tgaatccttg cgtcccgaag gacggagggtt caagcagagt 1493

Lys Glu Ala Pro

gagaagttaa aataccct

1511

<210> 12

<211> 484

<212> PRT

<213> Homo sapiens

<400> 12

Met Asp Glu Gly Ile Pro His Leu Gln Glu Arg Gln Leu Leu Glu His

1

5

10

15

Arg Asp Phe Ile Gly Leu Asp Tyr Ser Ser Leu Tyr Met Cys Lys Pro

20

25

30

Lys Arg Ser Met Lys Arg Asp Asp Thr Lys Val Ser Asp Thr Tyr Lys

35

40

45

Leu Pro His Arg Leu Ile Glu Lys Lys Arg Arg Asp Arg Ile Asn Glu

50

55

60

Cys Ile Ala Gln Leu Lys Asp Leu Leu Pro Glu His Leu Lys Leu Thr

65

70

75

80

Thr Leu Gly His Leu Glu Lys Ala Val Val Leu Glu Leu Thr Leu Lys

85

90

95

His Leu Lys Ala Leu Thr Ala Leu Thr Glu Gln Gln His Gln Lys Ile

100

105

110

Ile Ala Leu Gln Asn Gly Glu Arg Ser Leu Lys Ser Pro Ile Gln Ser

115

120

125

Asp Leu Asp Ala Phe His Ser Gly Phe Gln Thr Cys Ala Lys Glu Val

130

135

140

Leu Gln Tyr Leu Ser Arg Phe Glu Ser Trp Thr Pro Arg Glu Pro Arg
 145 150 155 160

Cys Val Gln Leu Ile Asn His Leu His Ala Val Ala Thr Gln Phe Leu
 165 170 175

Pro Thr Pro Gln Leu Leu Thr Gln Gln Val Pro Leu Ser Lys Gly Thr
 180 185 190

Gly Ala Pro Ser Ala Ala Gly Ser Ala Ala Ala Pro Cys Leu Glu Arg
 195 200 205

Ala Gly Gln Lys Leu Glu Pro Leu Ala Tyr Cys Val Pro Val Ile Gln
 210 215 220

Arg Thr Gln Pro Ser Ala Glu Leu Ala Ala Glu Asn Asp Thr Asp Thr
 225 230 235 240

Asp Ser Gly Tyr Gly Gly Glu Ala Glu Ala Arg Pro Asp Arg Glu Lys
 245 250 255

Gly Lys Gly Ala Gly Ala Ser Arg Val Thr Ile Lys Gln Glu Pro Pro
 260 265 270

Gly Glu Asp Ser Pro Ala Pro Lys Arg Met Lys Leu Asp Ser Arg Gly

275

280

285

Gly Gly Ser Gly Gly Gly Pro Gly Gly Gly Ala Ala Ala Ala Ala Ala

290

295

300

Ala Leu Leu Gly Pro Asp Pro Ala Ala Ala Ala Ala Leu Leu Arg Pro

305

310

315

320

Asp Ala Ala Leu Leu Ser Ser Leu Val Ala Phe Gly Gly Gly Gly Gly

325

330

335

Ala Pro Phe Pro Gln Pro Ala Ala Ala Ala Ala Pro Phe Cys Leu Pro

340

345

350

Phe Cys Phe Leu Ser Pro Ser Ala Ala Ala Ala Tyr Val Gln Pro Phe

355

360

365

Leu Asp Lys Ser Gly Leu Glu Lys Tyr Leu Tyr Pro Ala Ala Ala Ala

370

375

380

Ala Pro Phe Pro Leu Leu Tyr Pro Gly Ile Pro Ala Pro Ala Ala Ala

385

390

395

400

Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Phe Pro Cys

405

410

415

Leu Ser Ser Val Leu Ser Pro Pro Pro Glu Lys Ala Gly Ala Ala Ala

420

425

430

Ala Thr Leu Leu Pro His Glu Val Ala Pro Leu Gly Ala Pro His Pro

435

440

445

Gln His Pro His Gly Arg Thr His Leu Pro Phe Ala Gly Pro Arg Glu

450

455

460

Pro Gly Asn Pro Glu Ser Ser Ala Gln Glu Asp Pro Ser Gln Pro Gly

465

470

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Lys Glu Ala Pro

<210> 13

<211> 1421

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (74)..(1303)

<400> 13

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acagccattg aac atg gac gaa gga atc cct cat ttg caa gag aga cag 109

Met Asp Glu Gly Ile Pro His Leu Gln Glu Arg Gln

1

5

10

tta ctg gaa cat agg gat ttt ata gga ctg gac tat tcc tct ttg tat 157

Leu Leu Glu His Arg Asp Phe Ile Gly Leu Asp Tyr Ser Ser Leu Tyr

15

20

25

atg tgt aaa ccc aaa agg agc ttg aag cga gac gat acc aag gat acc 205

Met Cys Lys Pro Lys Arg Ser Leu Lys Arg Asp Asp Thr Lys Asp Thr

30

35

40

tac aag tta ccg cac aga tta ata gaa aag aag aga cga gac cga att 253

Tyr Lys Leu Pro His Arg Leu Ile Glu Lys Lys Arg Arg Asp Arg Ile

45

50

55

60

aat gaa tgc att gct cag ctg aaa gat tta ctg ccc gaa cat ctg aaa 301

Asn Glu Cys Ile Ala Gln Leu Lys Asp Leu Leu Pro Glu His Leu Lys

65

70

75

ttg aca aca ctg ggg cat ttg gag aaa gca gta gtc ttg gaa tta act 349

Leu Thr Thr Leu Gly His Leu Glu Lys Ala Val Val Leu Glu Leu Thr

80

85

90

tta aag cac ttg aaa gcg cta aca gcc tta act gag cag cag cat cag 397

Leu Lys His Leu Lys Ala Leu Thr Ala Leu Thr Glu Gln Gln His Gln

95

100

105

aag ata att gct tta cag aat ggg gag cgc tct ctg aaa tcg ccg gtc 445

Lys Ile Ile Ala Leu Gln Asn Gly Glu Arg Ser Leu Lys Ser Pro Val

110

115

120

cag gcc gac ttg gat gcg ttc cac tcg ggg ttt caa acc tgc gcc aaa 493

Gln Ala Asp Leu Asp Ala Phe His Ser Gly Phe Gln Thr Cys Ala Lys

125

130

135

140

gaa gtc ttg caa tac ctc gcg cgc ttt gag agc tgg aca ccc agg gag 541

Glu Val Leu Gln Tyr Leu Ala Arg Phe Glu Ser Trp Thr Pro Arg Glu

145

150

155

ccg cgc tgc gca cag ctc gtc agc cac ctg cat gcc gtg gcc acc cag 589

Pro Arg Cys Ala Gln Leu Val Ser His Leu His Ala Val Ala Thr Gln

160

165

170

ctc ctg acg cca cag gtg ccc tcc ggc agg ggc tct ggg cgc gcg ccc 637

Leu Leu Thr Pro Gln Val Pro Ser Gly Arg Gly Ser Gly Arg Ala Pro

175

180

185

tgc agc gcg ggg gct gcg gcc gcc tcg ggt ccc gag cgc gtc gcc cgc 685

Cys Ser Ala Gly Ala Ala Ala Ala Ser Gly Pro Glu Arg Val Ala Arg

190

195

200

tgc gtg ccg gtc atc cag cgg act cag ccc ggc acg gag ccg gaa cac 733

Cys Val Pro Val Ile Gln Arg Thr Gln Pro Gly Thr Glu Pro Glu His

205

210

215

220

gac acg gac acc gac agc ggc tac gga ggc gag gcg gag cag ggc cgc 781

Asp Thr Asp Thr Asp Ser Gly Tyr Gly Gly Glu Ala Glu Gln Gly Arg

225

230

235

gcg gcc gtc aag cag gag cca ccc ggg gac tcg tcg cct gcg ccc aag 829

Ala Ala Val Lys Gln Glu Pro Pro Gly Asp Ser Ser Pro Ala Pro Lys

240

245

250

agg ccg aag ctg gag gcg cgc ggc gcg ctc ctg ggc ccg gag ccc gcg 877

Arg Pro Lys Leu Glu Ala Arg Gly Ala Leu Leu Gly Pro Glu Pro Ala

255

260

265

ctg ctc ggc tcg ctc gtg gcg ctt ggc ggg ggc gcg ccc ttc gcg cag 925

Leu Leu Gly Ser Leu Val Ala Leu Gly Gly Gly Ala Pro Phe Ala Gln

270

275

280

ccc gct gcc gcg ccc ttc tgc ctg ccc ttc tat ctg ctg tcg ccg tcc 973

Pro Ala Ala Ala Pro Phe Cys Leu Pro Phe Tyr Leu Leu Ser Pro Ser

285

290

295

300

gcc gcc gcc tac gta cag ccc tgg cta gac aag agc ggc ctg gac aag 1021
 Ala Ala Ala Tyr Val Gln Pro Trp Leu Asp Lys Ser Gly Leu Asp Lys
 305 310 315

tat ctg tac ccc gcg gcg gcc gcg ccc ttc ccg ctg ctg tat ccc ggc 1069
 Tyr Leu Tyr Pro Ala Ala Ala Ala Pro Phe Pro Leu Leu Tyr Pro Gly
 320 325 330

atc cca gca gcg gcc gcc gct gct gct gcc gcc gct ttc cct tgc ttg 1117
 Ile Pro Ala Ala Ala Ala Ala Ala Ala Ala Ala Phe Pro Cys Leu
 335 340 345

tcg tcc gtg ctg tcg cca ccc ccg gag aag gcc ggc gcg acc gcc ggt 1165
 Ser Ser Val Leu Ser Pro Pro Pro Glu Lys Ala Gly Ala Thr Ala Gly
 350 355 360

gcc ccg ttc ctg gcg cac gag gtg gcg ccc ccg ggg ccg ctg cgc ccc 1213
 Ala Pro Phe Leu Ala His Glu Val Ala Pro Pro Gly Pro Leu Arg Pro
 365 370 375 380

cag cac gcg cat agc cgc acc cac ctg ccg cgc gct gtg aac ccg gag 1261
 Gln His Ala His Ser Arg Thr His Leu Pro Arg Ala Val Asn Pro Glu
 385 390 395

agc tct cag gaa gat gcc acg cag ccg gcc aag gac gcc ccc 1303
 Ser Ser Gln Glu Asp Ala Thr Gln Pro Ala Lys Asp Ala Pro

400

405

410

tgaacccagc attccttcca gaacagggca gggggctccc gaggagtcgc cgggtttcca 1363

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Met Asp Glu Gly Ile Pro His Leu Gln Glu Arg Gln Leu Leu Glu His

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5

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15

Arg Asp Phe Ile Gly Leu Asp Tyr Ser Ser Leu Tyr Met Cys Lys Pro

20

25

30

Lys Arg Ser Leu Lys Arg Asp Asp Thr Lys Asp Thr Tyr Lys Leu Pro

35

40

45

His Arg Leu Ile Glu Lys Lys Arg Arg Asp Arg Ile Asn Glu Cys Ile

50

55

60

Ala Gln Leu Lys Asp Leu Leu Pro Glu His Leu Lys Leu Thr Thr Leu

65

70

75

80

Gly His Leu Glu Lys Ala Val Val Leu Glu Leu Thr Leu Lys His Leu

85

90

95

Lys Ala Leu Thr Ala Leu Thr Glu Gln Gln His Gln Lys Ile Ile Ala

100

105

110

Leu Gln Asn Gly Glu Arg Ser Leu Lys Ser Pro Val Gln Ala Asp Leu

115

120

125

Asp Ala Phe His Ser Gly Phe Gln Thr Cys Ala Lys Glu Val Leu Gln

130

135

140

Tyr Leu Ala Arg Phe Glu Ser Trp Thr Pro Arg Glu Pro Arg Cys Ala

145

150

155

160

Gln Leu Val Ser His Leu His Ala Val Ala Thr Gln Leu Leu Thr Pro

165

170

175

Gln Val Pro Ser Gly Arg Gly Ser Gly Arg Ala Pro Cys Ser Ala Gly

180

185

190

Ala Ala Ala Ala Ser Gly Pro Glu Arg Val Ala Arg Cys Val Pro Val

195

200

205

Ile Gln Arg Thr Gln Pro Gly Thr Glu Pro Glu His Asp Thr Asp Thr

210

215

220

Asp Ser Gly Tyr Gly Gly Glu Ala Glu Gln Gly Arg Ala Ala Val Lys

225

230

235

240

Gln Glu Pro Pro Gly Asp Ser Ser Pro Ala Pro Lys Arg Pro Lys Leu

245

250

255

Glu Ala Arg Gly Ala Leu Leu Gly Pro Glu Pro Ala Leu Leu Gly Ser

260

265

270

Leu Val Ala Leu Gly Gly Gly Ala Pro Phe Ala Gln Pro Ala Ala Ala

275

280

285

Pro Phe Cys Leu Pro Phe Tyr Leu Leu Ser Pro Ser Ala Ala Ala Tyr

290

295

300

Val Gln Pro Trp Leu Asp Lys Ser Gly Leu Asp Lys Tyr Leu Tyr Pro

305

310

315

320

Ala Ala Ala Ala Pro Phe Pro Leu Leu Tyr Pro Gly Ile Pro Ala Ala

325

330

335

Ala Ala Ala Ala Ala Ala Ala Ala Phe Pro Cys Leu Ser Ser Val Leu

340

345

350

Ser Pro Pro Pro Glu Lys Ala Gly Ala Thr Ala Gly Ala Pro Phe Leu
 355 360 365

Ala His Glu Val Ala Pro Pro Gly Pro Leu Arg Pro Gln His Ala His
 370 375 380

Ser Arg Thr His Leu Pro Arg Ala Val Asn Pro Glu Ser Ser Gln Glu
 385 390 395 400

Asp Ala Thr Gln Pro Ala Lys Asp Ala Pro
 405 410

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<223> Description of Artificial Sequence:Artificially

Synthesized Primer Sequence

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

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